SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT:
 - (A) NAME: Jarl Wikberg
 - (B) STREET: Trillvaegen 13
 - (C) CITY: Umea
 - (E) COUNTRY: Sweden
 - (F) POSTAL CODE (ZIP): 905 92 Umea
 - (A) NAME: Vijay Chhajlani
 - (B) STREET: Stigbergsvaegen
 - (C) CITY: Uppsala
 - (E) COUNTRY: Sweden
 - (F) POSTAL CODE (ZIP): 752 42 Uppsala
- (ii) TITLE OF INVENTION: Human Melanocyte stimulating hormone receptor
- (iii) NUMBER OF SEQUENCES: 20
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox
 - (B) STREET: 1100 New York Ave., N.W.
 - (C) CITY: Washington
 - (D) STATE: D.C.
 - (E) COUNTRY: USA
 - (F) ZIP: 20005
 - (V) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-LOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/387,805
 - (B) FILING DATE: 21-FEB-95
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/DK93/00273
 - (B) FILING DATE: 20-AUG-93
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: DK 1046/92
 - (B) FILING DATE: 21-AUG-92
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: DK 1118/92
 - (B) FILING DATE: 10-SEP-92
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: DK 0528/93
 - (B) FILING DATE: 05-MAY-93
- (viii) ATTOFNEY/AGENT INFORMATION:

(A) NAME: Cimbala, Michele A.(B) PEGISTRATION NUMBER: 33,851(C) PEFERENCE/DOCKET NUMBER: 1102.0160000

	(ix)	(A)) TE	LEPHO	: and	(202	INFOI 2)371	1-26	00							
(2)	INFO	RMAT	IOII	FOR S	SEQ :	ID NO	o: 1	:								
	(i)	(A (B (C) LEI) TYI) STI	NGTH PE: 1 RANDI	: 12' nucl	70 ba eic a SS: o	doub!	pair	s							
	(ii)	MOL	ECUL	E TY	PE:	DNA	(cDN	A)								
	(ix)) 11A	ME/K	EY: ON:		.112	2								
	(xi)	SEQ	UENC	E DE	SCRI	PTIO	N: S	EQ I	CiN D	: 1:						
GGAG.	AGGG	TG T	GAGG	GCAG.	A TC	TGGG	GGTG	CCC	AGAT	GGA	AGGA	GGCA	.GG C	ATGG	GGGAC	60
ACCC	AAGG	cc c	CCTG	GCAG	C AC	CATG	AACT	AAG	CAGG	ACA	CCTG	GAGG	GG A	AGAA	CTGTG	120
GGGA	CCTG	GA G	GC CT	CCAA	.C GA	CTCC	TTCC	TGC	TTCC	TGG	ACAG	GACT	ATG Met	GCT Ala	GTG Val	177
CAG Gln	GGA Gly 5	TCC Ser	CAG Gln	AGA Arg	AGA Arg	CTT Leu 10	CTG Leu	GGC Gly	TCC Ser	CTC Leu	AAC Asn 15	TCC Ser	ACC Thr	CCC Pro	ACA Thr	225
GCC Ala 20	ATC Ile	CCC Pro	CAG Gln	CTG Leu	GGG Gly 25	CTG Leu	GCT Ala	GCC Ala	AAC Asn	CAG Gln 30	ACA Thr	GGA Gly	GCC Ala	CGG Arg	TGC Cys 35	273
CTG Leu	GAG Glu	GTG Val	TCC Ser	ATC Ile 40	TCT Ser	GAC Asp	GGG Gly	CTC Leu	TTC Phe 45	CTC Leu	AGC Ser	CTG Leu	GGG Gly	CTG Leu 50	GTG Val	321
AGC Ser	TTG Leu	GTG Val	GAG Glu 5,5	AAC Asn	GCG Ala	CTG Leu	GTG Val	GTG Val 60	GCC Ala	ACC Thr	ATC Ile	GCC Ala	AAG Lys 65	AAC Asn	CGG Arg	369
AAC Asn	CTG Leu	CAC His	TCA Ser	CCC Pro	ATG Met	TAC Tyr	TGC Cys 75	TTC Phe	ATC Ile	TGC Cys	TGC Cys	CTG Leu 80	GCC Ala	TTG Leu	TCG Ser	417
GAC Asp	CTG Leu 85	Leu	GTG Val	AGC Ser	GGG Gly	AGC Ser 90	AAC Asn	GTG Val	CTG Leu	GAG Glu	ACG Thr 95	GCC Ala	GTC Val	ATC Ile	CTC Leu	465
CTG Leu	CTG Leu	GAG Glu	GCC Ala	GGT Gly	GCA Ala	CTG Leu	GTG Val	GCC Ala	CGG Arg	GCT Ala	GCG Ala	GTG Val	CTG Leu	CAG Gln	CAG Gln	513

												-	
100		105					110					115	
CTG GAC AL	sn Val	ATT GAC Ile Asp 120	GTG Val	ATC Ile	ACC Thr	TGC Cys 125	AGC Ser	TCC Ser	ATG Met	CTG Leu	TCC Ser 130	AGC Ser	561
CTC TGC T	TC CTG (he Leu (135	GGC GCC Gly Ala	ATC Ile	GCC Ala	GTG Val 140	GAC Asp	CGC Arg	TAC Tyr	ATC Ile	TCC Ser 145	ATC Ile	TTC Phe	609
TAC GCA C Tyr Ala L 1	TG CGC ' eu Arg ' 50	TAC CAC Tyr His	AGC Ser	ATC Ile 155	GTG Val	ACC Thr	CTG Leu	CCG Pro	CGG Arg 160	GCG Ala	CGG Arg	CGA Arg	657
CGC GTT G Arg Val A 165	GCG GCC A	ATC TGG Ile Trp	GTG Val 170	GCC Ala	AGT Ser	GTC Val	GTC Val	TTC Phe 175	AGC Ser	ACG Thr	CTC Leu	TTC Phe	705
ATC GCC T Ile Ala T 180	AC TAC	GAC CAC Asp His 185	Val	GCC Ala	GTC Val	CTG Leu	CTG Leu 190	TGC Cys	CTC Leu	GTG Val	GTC Val	TTC Phe 195	753
TTC CTG G Phe Leu A	Ala Met	CTG GTG Leu Val 200	CTC Leu	ATG Met	GCC Ala	GTG Val 205	CTG Leu	TAC Tyr	GTC Val	CAC His	ATG Met 210	CTG Leu	801
GCC CGG G Ala Ang A	SCC TGC Ala Cys 215	CAG CAC	GCC Ala	CAG Gln	GGC Gly 220	ATC Ile	GCC Ala	CGG Arg	CTC Leu	CAC His 225	AAG Lys	AGG Arg	849
CAG CGC C Gln Arg E	CCG GTC Pro Val	CAC CAG	GGC Gly	TTT Phe 235	GGC Gly	CTT Leu	AAA Lys	GGC Gly	GCT Ala 240	GTC Val	ACC Thr	CTC Leu	897
ACC ATC C Thr Ile I 245	CTG CTG Leu Leu	GGC ATT	TTC Phe 250	TTC Phe	CTC Leu	TGC Cys	TGG Trp	GGC Gly 255	Pro	TTC Phe	TTC Phe	CTG Leu	945
CAT CTC A His Leu 7 260	ACA CTC Thr Leu	ATC GTC Ile Val 265	. Leu	TGC Cys	CCC Pro	GAG Glu	CAC His 270	CCC Pro	ACG Thr	TGC Cys	GGC Gly	TGC Cys 275	993
ATC TTC A	AAG AAC Lys Asn	TTC AAC Phe Asr 280	CTC Leu	TTT Phe	CTC Leu	GCC Ala 285	Leu	ATC Ile	ATC Ile	TGC Cys	AAT Asn 290	Ala	1041
ATC ATC (GAC CCC Asp Pro 295	CTC ATC	C TAC E Tyr	Ala	Phe	His	AGC Ser	GIn	i GLU	CTC Leu 305	Arg	AGG Arg	1089
ACG CTC . Thr Leu	AAG GAG Lys Glu 310	GTG CTC Val Let	G ACA ı Thr	TGC Cys 315	Ser	TGG Trp	TGA	(GCGC	GGT	GCAC	GCGC	TT	1139
TAAGTGTG	CT GGGC	AGAGGG 1	AGGTG	GTGA	TA TA	TGTG	TGGT	CTC	GTTC	CTG	TGTG	ACCCTG	1199
												CTCTGA	1259

AAGTGTTGAA G

(2)	INFORMATION	FOR	SEQ	ID	NO:	2:
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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 317 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: polypeptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser 10 15

Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
20 25 30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu 35

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala 50

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu 70 75 80

Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala 85 90 95

Val Ile Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val 100 105 110

Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met 115

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile 130 135 140

Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg 145 150 150

Ala Arg Arg Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser 165 170 175

Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu 180 185 190

Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val 195 200 205

His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu 210 215 220

His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala 225 230 235 240

Val	Thr	Leu	Thr	Ile 245	Leu	Leu	Gly	Ile	Phe 250	Phe	Leu	Cys	Trp	Gly 255	Pro	
Phe	Phe	Leu	His 260	Leu	Thr	Leu	Ile	Val 265	Leu	Cys	Pro	Glu	His 270	Pro	Thr	
Cys	Gly	Cys 275	Ile	Phe	Lys	Asn	Phe 280	Asn	Leu	Phe	Leu	Ala 285	Leu	Ile	Ile	
Cys	Asn 290	Ala	Ile	Ile	Asp	Pro 295	Leu	Ile	Tyr	Ala	Phe 300	His	Ser	Gln	Glu	
Leu 305	Arg	Arg	Thr	Leu	Lys 310	Glu	Val	Leu	Thr	Cys 315	Ser	Trp				
(2)	(i (ii) SE (, (((QUENCE DO TO LECU	CE C ENGT TPAN OPOL LE T	HARAGH: 3 nuc DEDN DGY:	CTERI 3 bas leic ESS: line DNA	ISTI se p aci sin ear (sy	CS: airs d gle nthe	tic)	o: 3	:					
GGG			TGTG													33
			TIO!I													
(2)) SE ((QUEN (A) I (B) T (C) S (D) T	CE C ENGT YPE: TRAL	HARA H: 3 nuc	CTER 5 ba :leic :ESS:	ISTI se p aci sin	CS: pairs	;							
			DLECU													
GGG			equen Aga							10: 4						35
(2)	INI (FORM	1OITA	I FCI	SEÇ	O ID	110:	5:								
	į)		(B) 5 (C) 5	LENG' LYPE STRAI	TH: 2 : nuc :IDEI	285 k cleid	base c ac: do:	pai: id uble	rs							
	(i:	i) M	OLEC	ULE '	TYPE	: DNA	A (P	CR-f.	ragm	ent)						
	(i:	×) F	EATU:		/KEY	: CD:	S									

(B) LOCATION: 1..285

(xi)	SEQUENCE	DESCRIPTION:	SEQ	ΙD	NO:	5:
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TTC Phe 1	TAC Tyr	GCA Ala	CTG Leu	CGC Arg 5	TAC Tyr	CAC His	AGC Ser	ATC Ile	GTG Val 10	ACC Thr	ATG Met	CGC Arg	CGC Arg	ACT Thr 15	GTG Val	48
GTG Val	GTG Val	CTT Leu	ACG Thr 20	GTC Val	ATC Ile	TGG Trp	ACG Thr	TTC Phe 25	TGC Cys	ACG Thr	GGG Gly	ACT Thr	GGC Gly 30	ATC Ile	ACC Thr	96
ATG Met	GTG Val	ATC Ile 35	TTC Phe	TCC Ser	CAT His	CAT His	GTG Val 40	CCC Pro	ACA Thr	GTG Val	ATC Ile	ACC Thr 45	TTC Phe	ACG Thr	TCG Ser	144
CTG Leu	TTC Phe 50	CCG Pro	CTG Leu	ATG Met	CTG Leu	GTC Val 55	TTC Phe	ATC Ile	CTG Leu	TGC Cys	CTC Leu 60	TAT Tyr	GTG Val	CAC His	ATG Met	192
TTC Phe 65	CTG Leu	CTG Leu	GCT Ala	CGA Arg	TCC Ser 70	CAC His	ACC Thr	AGG Arg	AAG Lys	ATC Ile 75	TCC Ser	ACC Thr	CTC Leu	CCC Pro	AGA Arg 80	240
GCC Ala	AAC Asn	ATG Met	AAA Lys	GGG Gly 85	GCC Ala	ATC Ile	ACC Thr	CTC Leu	ACC Thr 90	ATC Ile	CTG Leu	CTG Leu	GGC Gly	ATT Ile 95		285

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 95 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: polypeptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Met Arg Arg Thr Val

Val Val Leu Thr Val Ile Trp Thr Phe Cys Thr Gly Thr Gly Ile Thr 20 25 30

Met Val Ile Phe Ser His His Val Pro Thr Val Ile Thr Phe Thr Ser 35 40 45

Leu Phe Pro Leu Met Leu Val Phe Ile Leu Cys Leu Tyr Val His Met 50 55 60

Phe Leu Leu Ala Arg Ser His Thr Arg Lys Ile Ser Thr Leu Pro Arg 65 70 75 80

Ala Asn Met Lys Gly Ala Ile Thr Leu Thr Ile Leu Leu Gly Ile 85 90 95

(2)	INFC	RMAT	NOI	FOR	SEQ	ID N	10: 7	':								
	(i)	(<i>F</i> (E	A) LE B) TY C) ST	NGTE PE: RANI	I: 30 nucl EDNE	CTERI 06 ba leic CSS: line	se p acid doub	airs l	5							
	(ii)	MOI	LECUI	E TY	PE:	DNA	(PCF	≀-fra	agmer	nt)						
	(ix)	(I	ATURE A) NA B) LO	AME/F		CDS 13	306									
	(xi)	SEÇ	QUENC	CE DE	ESCRI	PTIC	211: 5	SEQ I	(D 1)(): 7:	:					
TTC Phe 1	TAC Tyr	GCA Ala	CTG Leu	CGC Arg 5	TAC Tyr	CAC His	AGC Ser	ATC Ile	GTG Val 10	ACG Thr	GCG Ala	AGG Arg	CGC Arg	TCA Ser 15	GGG Gly	48
GCC Ala	ATC Ile	ATC Ile	GCC Ala 20	GGC Gly	ATC Ile	TGG Trp	GCT Ala	TTC Phe 25	TGC Cys	ACG Thr	GGC Gly	TGC Cys	GGC Gly 30	ATT Ile	GTC Val	96
TTC Phe	ATC Ile	CTG Leu 35	TAC Tyr	TCA Ser	GAA Glu	TCC Ser	ACC Thr 40	TAC Tyr	GTC Va.l	ATC Ile	CTG Leu	TGC Cys 45	CTC Leu	ATC Ile	TCC Ser	144
ATG Met	TTC Phe 50	TTC Phe	GCT Ala	ATG Met	CTG Leu	TTC Phe 55	CTC Leu	CTG Leu	GTG Val	TCT Ser	CTG Leu 60	TAC Tyr	ATA Ile	CAC His	ATG Met	192
TTC Phe 65	CTC Leu	CTG Leu	GCG Ala	CGG Arg	ACT Thr 70	CAC His	GTC Val	AAG Lys	CGG Arg	ATC Ile 75	GCG Ala	CTC Leu	TGC Cys	CCG Pro	GGG Gly 80	240
CCA Pro	GCT Ala	CTG Leu	CGC Arg	GGC Gly 85	Arg	GGA Gly	CCA Pro	GCA Ala	TGC Cys 90	AGG Arg	GGC Gly	GCG Ala	GTC Val	ACC Thr 95	CTC Leu	288
			CTG Leu 100													306
(2)	INF	orma	TION	FOR	SEQ	ID	NC:	8:								
		(A) L B) T	ENGT YPE:	H: 1 ami		mino cid	TICS aci								
	(ii) MO	LECU	LE T	YPE:	pc·1	урер	tide								
	(xi) SE	QUEN	CE D	ESCR	IPTI	on:	SEQ	ID N	0: 8	:					

Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Ala Arg Arg Ser Gly 1 5 10 10 15

Ala	Ile	Ile	Ala 20	Gly	Ile	Trp	Ala	Phe 25	Cys	Thr	Gly	Cys	Gly 30	Ile	Val	
Phe	Ile	Leu 35	Tyr	Ser	Glu	Ser	Thr 40	туг	Val	Ile	Leu	Cys 45	Leu	Ile	Ser	
Met	Phe 50	Phe	Ala	Met	Leu	Phe 55	Leu	Leu	Val	Ser	Leu 60	Tyr	Ile	His	Met	
Phe 65	Leu	Leu	Ala	Arg	Thr 70	His	Val	Lys	Arg	Ile 75	Ala	Leu	Cys	Pro	Gly 80	
Pro	Ala	Leu	Arg	Gly 85	Arg	Gly	Pro	Ala	Cys 90	Arg	Gly	Ala	Val	Thr 95	Leu	
Thr	Ile	Leu	Leu 100	Gly	Ile											
(2)	INFO	PAMAC	HOI	FOF	SEQ	ID 1	10: 5	∋:								
	(i)	(<i>I</i> (I	A) Li B) TY C) ST	CE CH ENGTH (PE: FRANI DPOLO	H: 33 nucl DEDNE	l2 ba Leic ESS:	ase p acio douk	pairs d	5							
	(ii)	MOI	LECUI	LE TY	PE:	DNA	(PCF	₹~f.ra	agmer	nt)						
	(ix)	(]	,	E: AME/F OCATI			312									
		(<i>I</i>	3) I.(3) III	AME / F	[0]1:	13		SEQ I	ID NO	o: 9:	:					
	(XI)	(A (B SE) GCA	A) NA B) LO QUENO CTG	AME/F OCATI	ON: ESCRI TAC	1 PTIC CAC	ON: S	ATC	GTG	ACC	GTG					48
Phe 1 ACC	(XI) TAC Tyr TTG	(A (E SEQ GCA Ala ATC	A) NAS) LO QUENO CTG Leu GTG	AME/F DCATI CE IN CGT	ESCRITAC TAC Tyr	1 PTIC CAC His	ON: S AGC Ser GTC	ATC Ile	GTG Val 10	ACC Thr	GTG Val GTC	Arg TGT	Arg GGC	Ala 15 GTG	Leu	48 96
Phe 1 ACC Thr	(X1) TAC TYT TTG Leu	GCA Ala ATC Ile	A) NAS) LOS CTG Leu GTG Val 20	AME/FOCATION CE THE COST Arg	ESCRITAC TAC TYT ATC Ile	1 PTIC CAC His TGG Trp	AGC Ser GTC Val	ATC Ile TGC Cys 25	GTG Val 10 TGC Cys	ACC Thr GGC Gly	GTG Val GTC Val	Arg TGT Cys	GGC Gly 30	Ala 15 GTG Val	GTG Val	
Phe 1 ACC Thr TTC Phe	TAC Tyr TTG Leu ATC Ile	GCA Ala ATC Ile GTC Val 35	A) IM B) LO QUENO CTG Leu GTG Val 20 TAC Tyr	AME/FOCATION OF THE POST AND	ESCRITAC TAC Tyr ATC GAG Glu	1 PTIC CAC His TGG Trp	AGC Ser GTC Val AAA Lys 40	ATC Ile TGC Cys 25 ATG Met	GTG Val 10 TGC Cys GTC Val	ACC Thr GGC Gly ATT Ile	GTG Val GTC Val CTC	TGT Cys TGC Cys 45	GGC Gly 30 CTC Leu	Ala 15 GTG Val ATC Ile	GTG Val ACC Thr	96
Phe 1 ACC Thr TTC Phe ATG Met	TAC Tyr TTG Leu ATC Ile TTC Phe 50	GCA Ala ATC Ile GTC Val 35 TTC Phe	A) IM B) LO GUENO CTG Leu GTG Val 20 TAC Tyr GCC Ala	AME/FOCATION OF THE CONTROL OF THE C	ESCRITAC TAC TYR ATC Ile GAG Glu ATG Met	CAC His TGG Trp AGC Ser CTC Leu 55	AGC Ser GTC Val AAA Lys 40 CTC Leu	ATC Ile TGC Cys 25 ATG Met ATG Met	GTG Val 10 TGC Cys GTC Val GGC Gly	ACC Thr GGC Gly ATT Ile ACC Thr	GTG Val GTC Val GTG Val CTC Leu 60 GCA	TGT Cys TGC Cys 45 TAC Tyr	GGC Gly 30 CTC Leu GTG Val	Ala 15 GTG Val ATC Ile CAC His	GTG Val ACC Thr ATG Met	96 144

ACC CTC ACC ATC CTG CTG GGC ATT Thr Leu Thr Ile Leu Leu Gly Ile 100

- (2) INFORMATION FOR SEQ ID NO: 10:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 104 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: polypeptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Val Arg Arg Ala Leu 1 5 10 15

Thr Leu Ile Val Ala Ile Trp Val Cys Cys Gly Val Cys Gly Val Val 20 30

Phe Ile Val Tyr Ser Glu Ser Lys Met Val Ile Val Cys Leu Ile Thr 35 40 45

Met Phe Phe Ala Met Met Leu Leu Met Gly Thr Leu Tyr Val His Met 50 60

Phe Leu Phe Ala Arg Leu His Val Lys Arg Ile Ala Ala Leu Pro Pro 65 70 75 80

Ala Asp Gly Val Ala Prc Gln Gln His Ser Cys Met Lys Gly Ala Val

Thr Leu Thr Ile Leu Leu Gly Ile 100

- (2) INFORMATION FOR SEQ ID NO: 11:
 - (i) SEQUENCE CHAPACTERISTICS:
 - (A) LENGTH: 372 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (PCR-fragment)
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..372
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CTG TGT GTG ATC GCG CTG GAC CGG TAC ATC TCC ATC TTC TAC GCA CTG Leu Cys Val Ile Ala Leu Asp Arg Tyr Ile Ser Ile Phe Tyr Ala Leu 15

48

Arg	TAC Tyr	CAC His	AGC Ser 20	ATC Ile	GTG Val	ACC Thr	CTG Leu	CCG Pro 25	CGG Arg	GCG Ala	CCG Pro	GAA Glu	GCC Ala 30	GTT Val	GCG Ala	96
GCC Ala	ATC Ile	TGG Trp 35	GTG Val	GCC Ala	AGT Ser	GTC Val	GTC Val 40	TTC Phe	AGC Ser	ACG Thr	CTC Leu	TTC Phe 45	ATC Ile	GCC Ala	TAC Tyr	144
TAC Tyr	GAC Asp 50	CAC His	GTG Val	GCC Ala	GTC Val	CTG Leu 55	CTG Leu	TGC Cys	CTC Leu	GTG Val	GTC Val 60	TTC Phe	TTC Phe	CTG Leu	GCT Ala	192
ATG Met 65	CTG Leu	GTG Val	CTC Leu	ATG Met	GCC Ala 70	GTG Val	CTG Leu	TAC Tyr	GTC Val	CAC His 75	ATG Met	CTG Leu	GCC Ala	CGG Arg	GCC Ala 80	240
TGC Cys	CAG Gln	CAC His	GCC Ala	CAG Gln 85	GGC Gly	ATC Ile	GCC Ala	CGG Arg	CTC Leu 90	CAC His	AAG Lys	AGG Arg	CAG Gln	CGC Arg 95	CCG Pro	288
GTC Val	CAC His	CAG Gln	GGC Gly 100	TTT Phe	GGC Gly	CTT Leu	AAA Lys	GGC Gly 105	GCT Ala	GTC Val	ACC Thr	CTC Leu	ACC Thr 110	ATC Ile	CTG Leu	336
	GGC Gly															372
(2)	INF	ORMA'	LION	FOR	SEQ	ID 1	10:	12:								
(2)		(i) (i) (i)	SEQUI A) LI B) T	ENCE ENGT: YPE:	CHAI H: 1:	ID RACTI 24 am no ac line	ERIS' mino cid	rics								
(2)		(i) (i) (i) (i)	SEQUI A) LI B) T	ENCE ENGT: YPE: OPOL	CHAI H: 1: ami: OGY:	RACTI 24 ai no ac	ERIS' mino cid ear	rics aci								
(2)	(ii	(i) (i) (i) (i) (i)	SEQUI A) LI B) T D) T LECU	ENCE ENGT: YPE: OPOL	CHAI H: 1: ami: OGY: YPE:	RACTI 24 am no ao lino pro	ERIS' mino cid ear tein	rics aci	ds	o: 1:	2:					
	(ii	(i) ; (i) (i) (i)) MO	SEQUI A) LI B) T D) T LECU	ENCE ENGT: YPE: OPOL LE T	CHAI H: 1: ami: OGY: YPE: ESCR	RACTI 24 am no ac line pro	ERIST mino cid ear tein	rics aci	ds ID N			Phe	Tyr	Ala 15	Leu	
Leu 1	(ii (xi	(i) ; (i) (i)) MO) SE Val	SEQUIA) LIB) TO	ENCE ENGT: YPE: OPOL LE T CE D Ala 5	CHAI H: 1: amin OGY: YPE: ESCR	RACTI 24 am no ac line pro	ERIS' mino cid ear tein ON:	rics aci seQ Tyr	ID N Ile 10 Arg	Ser	Ile			15		
Leu 1 Arg	(ii (xi Cys	(i) ; (i) (i) (i)) MO) SE Val	SEQUIA) LIB) TO TO TO THE CU QUEN Ser 20 Val	ENCE ENGT: YPE: OPOL LE T CE D Ala 5	CHAN H: 1: amin OGY: YPE: Leu Val	RACTI 24 am no ac line pro IPTI Asp	ERIS' mino cid ear tein ON: Arg	FICS aci SEQ Tyr Pro 25 Phe	ID N Ile 10 Arg	Ser	Ile Pro	Glu	Ala 30 Ile	Val		
Leu 1 Arg	(ii (xi Cys	(i) ;	SEQUENT D) TO LECU QUEN Ser 20 Val	ENCE ENGT: YPE: OPOL LE T CE D Ala 5	CHAN H: 1: amin OGY: YPE: ESCR Leu Val	RACTI 24 and	ERIST mino cid ear tein ON: Arg Leu Val 40 Leu	FICS aci SEQ Tyr Pro 25 Phe	ID N Ile 10 Arg Ser	Ser Ala Thr	Ile Pro Leu	Glu Phe 45	Ala 30 Ile	Val Ala	Ala Tyr	
Leu 1 Arg Ala	(ii (xi Cys Tyr Ile Asp 50	(i) ; (ii) ; (ii) ; (iii) ; (iiii) ; (iiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiii	SEQUIA) LIB) TO LECU QUEN 20 Val	ENCE ENGT: YPE: OPOL LE T CE D Ala 5	CHAN H: 1: amin OGY: YPE: YPE: Leu Val	RACTI 24 and no accompany 1 production 1 PTI Asp Thr Val Leu 55	ERIST mino cid ear tein ON: Arg Leu Val 40 Leu	FICS aci SEQ Tyr Pro 25 Phe	ID No Ile 10 Arg	Ser Ala Thr	Pro Leu Val 60 Met	Glu Phe 45 Phe	Ala 30 Ile Phe	Val Ala Leu	Ala Tyr	

Val His Gln Gly Phe Gly Leu Lys Gly Ala Val Thr Leu Thr Ile Leu 100 105 110	
Leu Gly Ile Phe Thr Val Ser Trp Arg Pro Phe Phe 115 120	
(2) INFORMATION FOR SEQ ID NO: 13:	
 (i) SEQUENCE CHAPACTEPISTICS: (A) LENGTH: 35 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCPIPTION: SEQ ID NO: 13:	
GGGAATTCTA CGCACTGCGC TACCACAGCA TCGTG	35
(2) INFORMATION FOR SEC ID NO: 14:	
 (i) SEQUENCE CHAFACTERISTICS: (A) LENGTH: 34 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (synthetic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:	
GGGGATCCAA TGCCCAGCAG GATGGTGAGG GTGA	34
(2) INFORMATION FOR SEQ ID NO: 15:	
 (i) SEQUENCE CHAPACTERISTICS: (A) LENGTH: 1650 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(11) MOLECULE TYPE: DNA (CDNA)	
(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 6161590	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:	
CTTGAGGAGA ATGTCGTGCA GTAGCCTTAG GAATGTGAAC ATTGGGAGAC TGGCTGGGAT	60
TTTGTAGGTT ATGAGAAGGG GACACTTATG ATATGTGAAC TTGAGCCCAG GAGAGAAGCC	120
ATAAAAAGTG AAACTGTCCT GGGCACTTGG AGGTGAGTGT CTCTCTAGTA AGATGCATGT	180

GAAAGGCCTG GGAGCTGAAA GCAAGGAGAG CAGAAGAGGC TGGTGAAGAT TCTAATCTGC	240
GTGTCCAGGG GCACTCTTCC AGGTCTCAGG AACGCAGGTC AGAATGTGCA AGCCAGCTGC	300
CGGGCACGTG GCTCACCCCT GTAGTACCAG CACTTTGGGA GGCTGAGAGA GAAGATCGCT	360
TGTGGCCAGG AGTTTGAGAC CAGACTGGGG CTTCATAGGG AGACCCTGTC TCTTAAAAAA	420
AAAAAAAAA AAGGACTGAG TGAGCCGAGC CCAGTCCTCT CATGCACTGT GTCATTCATC	480
CCCTTTCTTA GGCTGTGTTG GTTCTAGGCT AGCTGCTGTC TTTCTTTGGT AGGCTGCTAA	540
CCTCTTTGGA TTGTGAATTT AAAACATGTT TTACAGTAAA TTTGCTGCCA AGACAAGAGG	600
TGTATTTCTC CAGCA ATG AAT TCC TCA TTT CAC CTG CAT TTC TTG GAT CTC Met Asn Ser Ser Phe His Leu His Phe Leu Asp Leu 1 5 10	÷5 5 1
AAC CTG AAT GCC ACA GAG GGC AAC CTT TCA GGA CCC AAT GTC AAA AAC Asn Leu Asn Ala Thr Glu Gly Asn Leu Ser Gly Pro Asn Val Lys Asn 15	ъ́∄9
AAG TCT TCA CCA TGT GAA GAC ATG GGC ATT GCT GTG GAG GTG TTT CTC Lys Ser Ser Pro Cyn Glu Asi Met Gly Ile Ala Val Glu Val Phe Leu 30 35 40	7.17
ACT CTG GGT GTC ATC AGC CTC TTG GAG AAC ATC TTG GTC ATA GGG GCC Thr Leu Gly Val Ile Ser Leu Leu Glu Asn Ile Leu Val Ile Gly Ala 45	795
ATA GTG AAG AAC AAA AAC CTG CAC TCC CCC ATG TAC TTC TTC GTG TGC Ile Val Lys Asn Lys Asn Leu His Ser Pro Met Tyr Phe Phe Val Cys 65	343
AGC CTG GCA GTG GCG GAC ATG CTG GTG AGC ATG TCC AGT GCC TGG GAG Ser Leu Ala Val Ala Asp Met Leu Val Ser Met Ser Ser Ala Trp Glu 80 85 90	891
ACC ATC ACC ATC TAC CTA CTC AAC AAC AAG CAC CTA GTG ATA GCA GAC Thr Ile Thr Ile Tyr Leu Leu Asn Asn Lys His Leu Val Ile Ala Asp 95 100 105	939
GCC TTT GTG CGC CAC ATT GAC AAT GTG TTT GAC TCC ATG ATC TGC ATT Ala Phe Val Arg His Ile Asp Asn Val Phe Asp Ser Met Ile Cys Ile 110 115 120	987
TCC GTG GTG GCA TCC ATG TGC AGC TTA CTG GCC ATT GCA GTG GAT AGG Ser Val Val Ala Ser Met Cys Ser Leu Leu Ala Ile Ala Val Asp Arg 125 130 135	1035
TAC GTC ACC ATC TTC TAC GCC CTG CGC TAC CAC CAC ATC ATG ACG GCG Tyr Val Thr Ile Phe Tyr Ala Leu Arg Tyr His His Ile Met Thr Ala 145 150 155	1083
AGG CGC TCA GGG GCC ATC ATC GCC GGC ATC TGG GCT TTC TGC ACG GGC Arg Arg Ser Gly Ala Ile Ile Ala Gly Ile Trp Ala Phe Cys Thr Gly 160 165 170	1131

TGC Cys	GGC Gly	ATT Ile 175	GTC Val	TTC Phe	ATC Ile	CTG Leu	TAC Tyr 180	TCA Ser	GAA Glu	TCC Ser	ACC Thr	TAC Tyr 185	GTC Val	ATC Ile	CTG Leu	1179
			TCC Ser												CTG Leu	1227
			ATG Met													1275
CTC Leu	TGC Cys	CCG Pro	GGG Gly	CCA Pro 225	GCT Ala	CTG Leu	CGC Arg	GGC Gly	AGA Arg 230	GGA Gly	CCA Pro	GCA Ala	TGG Trp	CAG Gln 235	GGC Gly	1323
GCG Ala	GTC Val	ACC Thr	GTC Val 240	ACC Thr	ATG Met	CTG Leu	CTG Leu	GGC Gly 245	GTG Val	TTT Phe	ACC Thr	GTG Val	TGC Cys 250	TGG Trp	GCC Ala	1371
CCG Pro	TTC Phe	TTC Phe 255	CTT Leu	CAT His	CTC Leu	ACT Thr	TTA Leu 260	ATG Met	CTT Leu	TCT Ser	TGC Cys	CCT Fro 265	CAG Gln	AAC Asn	CTC Leu	1419
			CGC Arg												ATC Ile	1467
ATG Met 285	TGT Cys	AAT Asn	TCC Ser	GTG Val	ATG Met 290	GAC Asp	CCT Pro	CTC Leu	ATA Ile	ТАТ Туг 295	GCC Ala	TTC Phe	cgc Arg	AGC Ser	CAA Gln 300	1515
GAG Glu	ATG Met	CGG Arg	AAG Lys	ACC Thr 305	TTT Phe	AAG Lys	GAG Glu	ATT Ile	ATT Ile 310	TGC Cys	TGC Cys	CGT Arg	GGT Gly	TTC Phe 315	AGG Arg	1563
			AGC Ser 320						TAA	CGAC	AAA	GTGC'	rcct(CT		1610
CTG	TGGC'	TCT	GTTC'	TCCT'	TT G'	TTTG	CTCA	C CT	ATGA	CAAA						1650

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 325 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (11) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Met Asn Ser Ser Phe His Leu His Phe Leu Asp Leu Asn Leu Asn Ala 1 5 10 15

Thr Glu Gly Asn Leu Ser Gly Pro Asn Val Lys Asn Lys Ser Ser Pro

			20					25					30		
Cys	Glu	Asp 35	Met	Gly	Ile	Ala	Val 40	Glu	Val	Phe	Leu	Thr 45	Leu	Gly	Val
Ile	Ser 50	Leu	Leu	Glu	Asn	Ile 55	Leu	Val	Ile	Gly	Ala 60	Ile	Val	Lys	Asn
Lys 65	Asn	Leu	Hıs	Ser	Pro 70	Met	Tyr	Phe	Phe	Val 75	Cys	Ser	Leu	Ala	Val 80
Ala	Asp	Met	Leu	Val 85	Ser	Met	Ser	Ser	Ala 90	Trp	Glu	Thr	Ile	Thr 95	Ile
Tyr	Leu	Leu	Asn 100	Asn	Lys	His	Leu	Val 105	Ile	Ala	Asp	Ala	Phe 110	Val	Arg
His	Ile	Asr 115	Asn	Val	Phe	Asp	Ser 120	Met	Ile	Cys	Ile	Ser 125	Val	Val	Ala
Ser	Met 130	Сує	Ser	Leu	Leu	Ala 135	Ile	Ala	Val	Asp	Arg 140	Tyr	Val	Thr	Ile
Phe 145	Tyr	Alā	Leu	Arg	Tyr 150	His	His	Ile	Met	Thr 155	Ala	Arg	Arg	Ser	Gly 160
Ala	Ile	Ile	Ala	Gly 165	Ile	Trp	Ala	Phe	Cys 170	Thr	Gly	Cla	Gly	11e 175	Val
Phe	Ile	Leu	Tyr 180	Ser	Glu	Ser	Thr	Tyr 185	Val	Ile	Leu	Cys	Leu 190	Ile	Ser
Met	Phe	Phe 195	Ala	Met	Leu	Phe	Leu 200	Leu	Val	Ser	Leu	Tyr 205	Ile	His	Met
Phe	Leu 210	Leu	Ala	Arg	Thr	His 215	Val	Lys	Arg	Ile	Ala 220	Leu	Cys	Pro	Gly
Pro 225	Ala	Leu	Arg	Gly	Arg 230		Pro	Ala	Trp	Gln 235	Gly	Ala	Val	Thr	Val 240
Thr	Met	Leu	Leu	Gly 245	Val	Phe	Thr	Val	Cys 250	Trp	Ala	Pro	Phe	Phe 255	Leu
His	Leu	Thr	Leu 260	Met	Leu	Ser	Cys	Pro 265		Asn	Leu	Туr	Cys 270	Ser	Arg
Phe	Met	Ser 275	His	Phe	Asn	Met	Tyr 280		Ile	Leu	Ile	Met 285	Cys	Asn	Ser
Val	Met 290		Pro	Leu	Ile	Tyr 295	Ala	Phe	Arg	Ser	Gln 300	Glu	Met	Arg	Lys
Thr 305		Lys	Glu	Ile	Ile 310		Cys	Arg	Gly	Phe 315		Ile	Ala	Cys	Ser 320

Phe Pro Arg Arg Asp 325

(2)	INFORMATION FOR SEQ ID NO: I/:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: DNA (synthetic)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO 17:	
GGA <i>I</i>	AGCTTTC TTTGGTAGGC TG	22
(2)	INFORMATION FOR SEQ ID NO: 18:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: DNA (synthetic)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:	
GGT	CTAGAGC CACAGAGAGG AG	22
(2)	INFORMATION FOR SEQ ID NO: 19:	
(2)		
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: DNA (synthetic)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:	
CTG	CATTTCT TGGATCT	17
(2)	INFORMATION FOR SEQ ID NO: 20:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: DNA (synthetic)	
	(xi) SEQUENCE DESCRIPTION: SEO ID NO: 20:	